

FIGURE 1

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GAGCTCGGAT CCACTACTCG ACCCACGCGT CCGGCCAGGA CCTCTGTGAA CCGGTCGGGG	60
CGGGGGCCGC CTGGCCGGGA GTCTGCTCGG CGGTGGGTGG CCGAGGAAGG GAGAGAACGA	120
TCGCGGAGCA GGGCGCCCGA ACTCCGGGCG CCGCGCC ATG CGC CGG GCC AGC CGA	175
Met Arg Arg Ala Ser Arg	
1 5	
GAC TAC GGC AAG TAC CTG CGC AGC TCG GAG GAG ATG GGC AGC GGC CCC	223
Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro	
10 15 20	
GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT	271
Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala	
25 30 35	
CCG GCG CCG CCA CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG	319
Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser <u>Met Phe Leu Ala Leu Leu</u>	
40 45 50	
GGG CTG GGA CTG GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC	367
<u>Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr</u>	
55 60 65 70	
TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC	415
Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His	
75 80 85	
TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC	463
Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp	
90 95 100	
TCG ACT CTG GAG AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG	511
Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met	
105 110 115	
AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG	559
Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val	
120 125 130	
GGG CCA CAG CGC TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG	607
Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp	
135 140 145 150	
TTG GAT GTG GCC CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC	655
Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His	
155 160 165	
CTC ACC ATC AAT GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT	703
Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr	
170 175 180	

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FIGURE 1 (Con't)

CTG TCC TCT TGG TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG	751
Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser <u>Asn</u> Met	
185 190 195	
ACG TTA AGC AAC GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC	799
Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr	
200 205 210	
CTG TAC GCC AAC ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA	847
Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val	
215 220 225 230	
CCT ACA GAC TAT CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC	895
Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile	
235 240 245	
AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC	943
Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys <u>Asn</u>	
250 255 260	
TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA	991
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly	
265 270 275	
TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC	1039
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser <u>Asn</u>	
280 285 290	
CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC	1087
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe	
295 300 305 310	
AAA GTT CAG GAC ATA GAC T GAGACTCATT TCGTGGGAACA TTAGCATGGA	1136
Lys Val Gln Asp Ile Asp	
315	
TGTCCTAGAT GTTTGGAAAC TTCTTAAAAA ATGGATGATG TCTATACATG TGTAAGACTA	1196
CTAAGAGACA TGGCCACCGG TGTATGAAAC TCACAGCCCT CTCTCTTGAG CCTGTACAGG	1256
TTGTGTATAT GTAAAGTCCA TAGGTGATGT TAGATTCATG GTGATTACAC AACGGTTTTA	1316
CAATTTTGTA ATGATTTCCCT AGAATTGAAC CAGATTGGGA GAGGTATTCC GATGCTTATG	1376
AAAACTTAC ACGTGAGCTA TGGAAGGGGG TCACAGTCTC TGGGTCTAAC CCCTGGACAT	1436
GTGCCACTGA GAACCTTGAA ATTAAGAGGA TGCCATGTCA TTGCAAAGAA ATGATAGTGT	1496
GAAGGGTTAA GTTCTTTTGA ATTGTTACAT TGCGCTGGGA CCTGCAAATA AGTTCTTTTT	1556

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# FIGURE 1 (Con't)

TTCTAATGAG	GAGAGAAAAA	TATATGTATT	TTTATATAAT	GTCTAAAGTT	ATATTTTCAGG	1616
TGTAATGTTT	TCTGTGCAAA	GTTTTGTAAA	TTATATTTGT	GCTATAGTAT	TTGATTCAAA	1676
ATATTTAAAA	ATGTCTCACT	GTTGACATAT	TTAATGTTTT	AAATGTACAG	ATGTATTTAA	1736
CTGGTGCACT	TTGTAATTCC	CCTGAAGGTA	CTCGTAGCTA	AGGGGGCAGA	ATACTGTTTC	1796
TGGTGACCAC	ATGTAGTTTA	TTTCTTTATT	CTTTTTTAAC	TAATAGAGTC	TTCAGACTTG	1856
TCAAACTAT	GCAAGCAAAA	TAAATAAATA	AAAATAAAAT	GAATACCTTG	AATAATAAGT	1916
AGGATGTTGG	TCACCAGGTG	CCTTTCAAAT	TTAGAAGCTA	ATTGACTTTA	GGAGCTGACA	1976
TAGCCAAAAA	GGATACATAA	TAGGCTACTG	AAATCTGTCA	GGAGTATTTA	TGCAATTATT	2036
GAACAGGTGT	CTTTTTTTAC	AAGAGCTACA	AATTGTAAAT	TTTGTTTCTT	TTTTTTCCCA	2096
TAGAAAATGT	ACTATAGTTT	ATCAGCCAAA	AAACAATCCA	CTTTTTTAATT	TAGTGAAAGT	2156
TATTTTATTA	TACTGTACAA	TAAAAGCATT	GTCTCTGAAT	GTTAATTTTT	TGGTACAAAA	2216
AATAAATTTG	TACGAAAACC	TGAAAAAAA	AAAAAATAAA	AAAAAAGGG	CGGCCGCTCT	2276
AGAGGGCCCT	ATTCTATAG					2295

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## Expression of 32D-F3 in COS-7 Cells

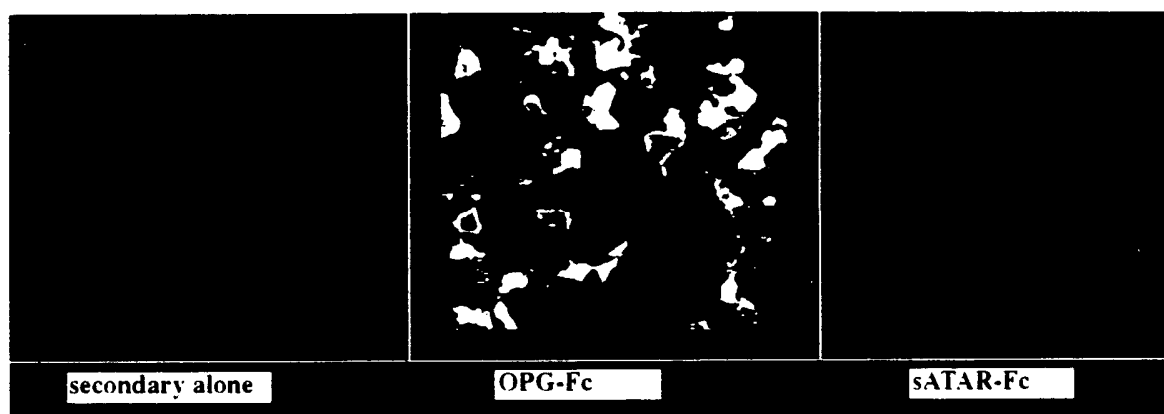


FIGURE 2

# OPG Binding Protein Expression in Human Tissues

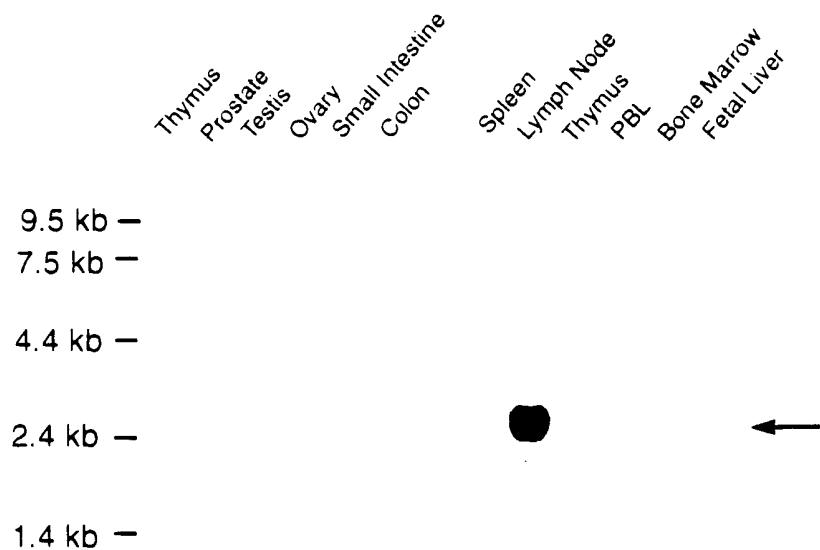


FIGURE 3

FIGURE 4

10 30 50  
 AAGCTTGGTACCGAGCTCGGATCCACTACTCGACCCACGCGTCCGCGCGCCCCAGGAGCC  
 70 90 110  
 AAAGCCGGGCTCCAAGTCGGCGCCCCACGTCGAGGCTCCGCCGAGCCTCCGGAGTTGGC  
 130 150 170  
 CGCAGACAAGAAGGGGAGGGAGCGGGAGAGGGAGGAGAGCTCCGAAGCGAGAGGGCCGAG  
 190 210 230  
 CGCCATGCGCCGCGCCAGCAGAGACTACACCAAGTACCTGCGTGGCTCGGAGGAGATGGG  
 M R R A S R D Y T K Y L R G S E E M G  
 250 270 290  
 CGGCGGCCCCGGAGCCCCGCACGAGGGCCCCCTGCACGCCCCGCCCGCCCTGCGCCGCA  
 G G P G A P H E G P L H A P P P P A P H  
 310 330 350  
 CCAGCCCCCGCCGCTCCCGCTCCATGTTCTGCGCCCTCCTGGGGCTGGGGCTGGGCCA  
 Q P P A A S R S M F V A L L G L G L G Q  
 370 390 410  
 GGTGTCTGCAGCGTCGCCCTGTTCTTCTATTTCAGAGCGCAGATGGATCCTAATAGAAT  
 V V C S V A L F F Y F R A Q M D P N R I  
 430 450 470  
 ATCAGAAGATGGCACTCACTGCATTTATAGAATTTTGAGACTCCATGAAAATGCAGATTT  
 S E D G T H C I Y R I L R L H E N A D F  
 490 510 530  
 TCAAGACACAACCTCTGGAGAGTCAAGATACAAAATTAATACCTGATTCATGTAGGAGAAT  
 Q D T T L E S Q D T K L I P D S C R R I  
 550 570 590  
 TAAACAGGCCTTTCAAGGAGCTGTGCAAAAGGAATTACAACATATCGTTGGATCACAGCA  
 K Q A F Q G A V Q K E L Q H I V G S Q H  
 610 630 650  
 CATCAGAGCAGAGAAAGCGATGGTGGATGGCTCATGGTTAGATCTGGCCAAGAGGAGCAA  
 I R A E K A M V D G S W L D L A K R S K  
 670 690 710  
 GCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTGGTTC  
 L E A Q P F A H L T I N A T D I P S G S  
 730 750 770  
 CCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCAACAT  
 H K V S L S S W Y H D R G W A K I S N M  
 790 810 830  
 GACTTTTAGCAATGGAAAATAATAGTTAATCAGGATGGCTTTTATTACCTGTATGCCAA  
 T F S N G K L I V N Q D G F Y Y L Y A N  
 850 870 890  
 CATTTGCTTTCGACATCATGAACTTCAGGAGACCTAGCTACAGAGTATCTTCAACTAAT  
 I C F R H H E T S G D L A T E Y L Q L M  
 910 930 950  
 GGTGTACGTCACTAAAACCAGCATCAAAATCCCAAGTTCTCATACCCTGATGAAAGGAGG  
 V Y V T K T S I K I P S S H T L M K G G  
 970 990 1010

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 064139 " 134490

# FIGURE 4

AAGCACCAAGTATTGGTCAGGGAATTCTGAATTCCATTTTTATTCCATAAACGTTGGTGG  
 S T K Y W S G N S E F H F Y S I N V G G  
  
 1030 1050 1070  
 ATTTTTTAAGTTACGGTCTGGAGAGGAAATCAGCATCGAGGTCTCCAACCCCTCCTTACT  
 F F K L R S G E E I S I E V S N P S L L  
  
 1090 1110 1130  
 GGATCCGGATCAGGATGCAACATACTTTGGGGCTTTTAAAGTTCGAGATATAGATTGAGC  
 D P D Q D A T Y F G A F K V R D I D  
  
 1150 1170 1190  
 CCCAGTTTTTGGAGTGTTATGTATTTCTGATGTTTGGAAACATTTTTTAAACAAGCC  
  
 1210 1230 1250  
 AAGAAAGATGTATATAGGTGTGTGAGACTACTAAGAGGCATGGCCCCAACGGTACACGAC  
  
 1270 1290 1310  
 TCAGTATCCATGCTCTTGACCTTGTAAGAACACGCGTATTTACAGCCAGTGGGAGATGT  
  
 1330 1350 1370  
 TAGACTCATGGTGTGTTACACAATGGTTTTTAAATTTGTAATGAATTCCTAGAATTAAA  
  
 1390 1410 1430  
 CCAGATTGGAGCAATTACGGGTTGACCTTATGAGAAACTGCATGTGGGCTATGGGAGGGG  
  
 1450 1470 1490  
 TTGGTCCCTGGTCATGTGCCCCCTTCGCAGCTGAAGTGGAGAGGGTGTCTAGCGCAAT  
  
 1510 1530 1550  
 TGAAGGATCATCTGAAGGGGCAAATTCCTTTGAATTGTTACATCATGCTGGAACCTGCAA  
  
 1570 1590 1610  
 AAAATACTTTTTCTAATGAGGAGAGAAAATATATGTATTTTTATATAATATCTAAAGTTA  
  
 1630 1650 1670  
 TATTTTCAGATGTAATGTTTTCTTTGCAAAGTATTGTAAATTATATTTGTGCTATAGTATT  
  
 1690 1710 1730  
 TGATTCAAAATATTTAAAAATGTCTTGCTGTTGACATATTTAATGTTTTAAATGTACAGA  
  
 1750 1770 1790  
 CATATTTAACTGGTGCACTTTGTAAATTCCTGGGGAAAACCTGCAGCTAAGGAGGGGAA

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# FIGURE 4

1810	1830	1850
AAAAATGTTGTTTCCTAATATCAAATGCAGTATATTTCTTCGTTCTTTTAAAGTTAATAG		
1870	1890	1910
ATTTTTTCAGACTTGTCAAGCCTGTGCAAAAAAATTAAAATGGATGCCTTGAATAATAAG		
1930	1950	1970
CAGGATGTTGGCCACCAGGTGCCTTTCAAATTTAGAACTAATTGACTTTAGAAAGCTGA		
1990	2010	2030
CATTGCCAAAAAGGATACATAATGGGCCACTGAAATCTGTCAAGAGTAGTTATATAATTG		
2050	2070	2090
TTGAACAGGTGTTTTCCACAAGTGCCGCAAATTGTACCTTTTTTTTTTTTTTCAAATAG		
2110	2130	2150
AAAAGTTATTAGTGGTTTATCAGCAAAAAAGTCCAATTTTAATTTAGTAAATGTTATCTT		
2170	2190	2210
ATACTGTACAATAAAAAACATTGCCTTTGAATGTTAATTTTTTGGTACAAAAATAAATTTA		
2230	2250	2270
TATGAAAAAAAAAAAAAGGGCGCGCTCTAGAGGGCCCTATTCTATAG		

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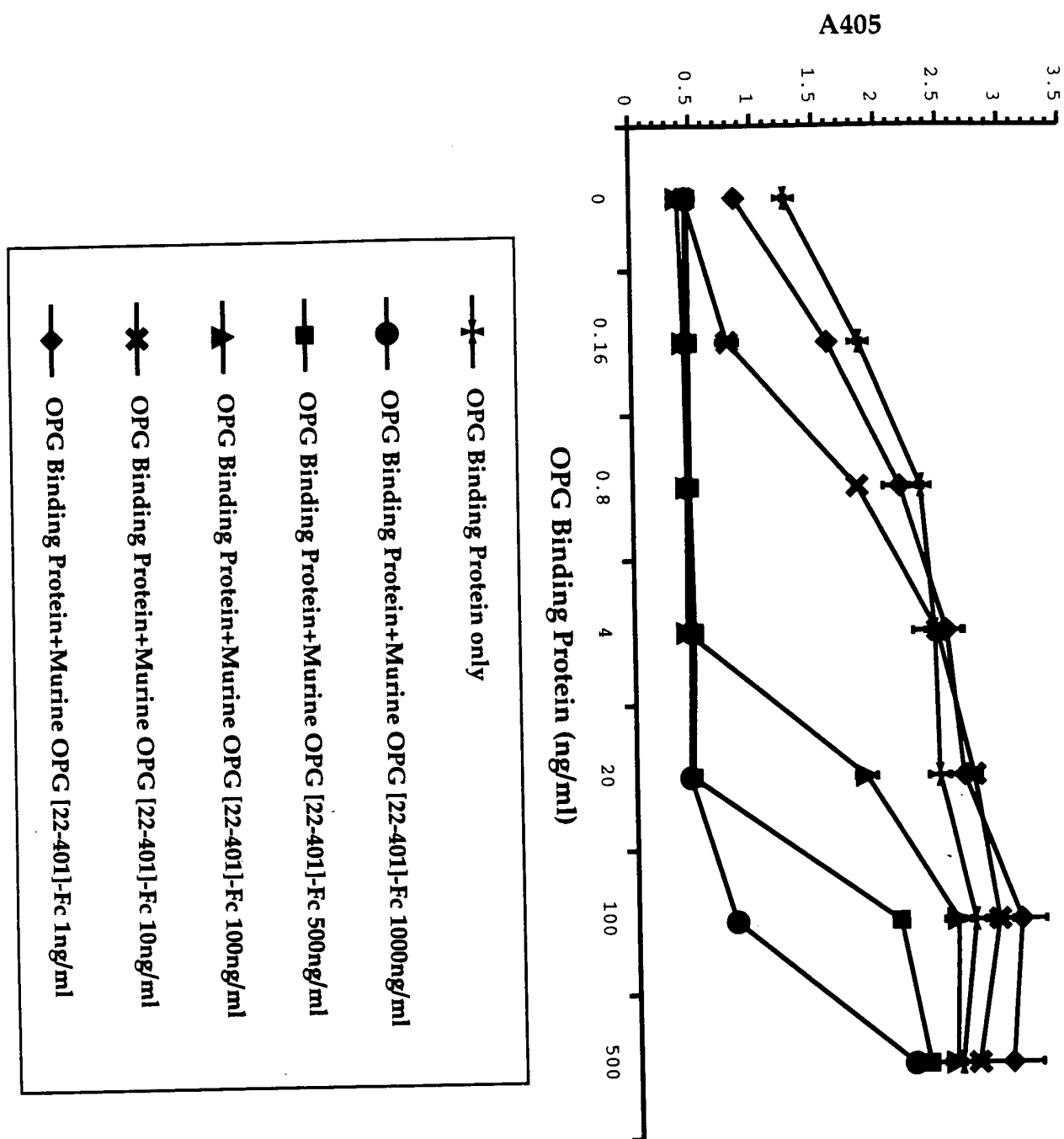


FIGURE 5

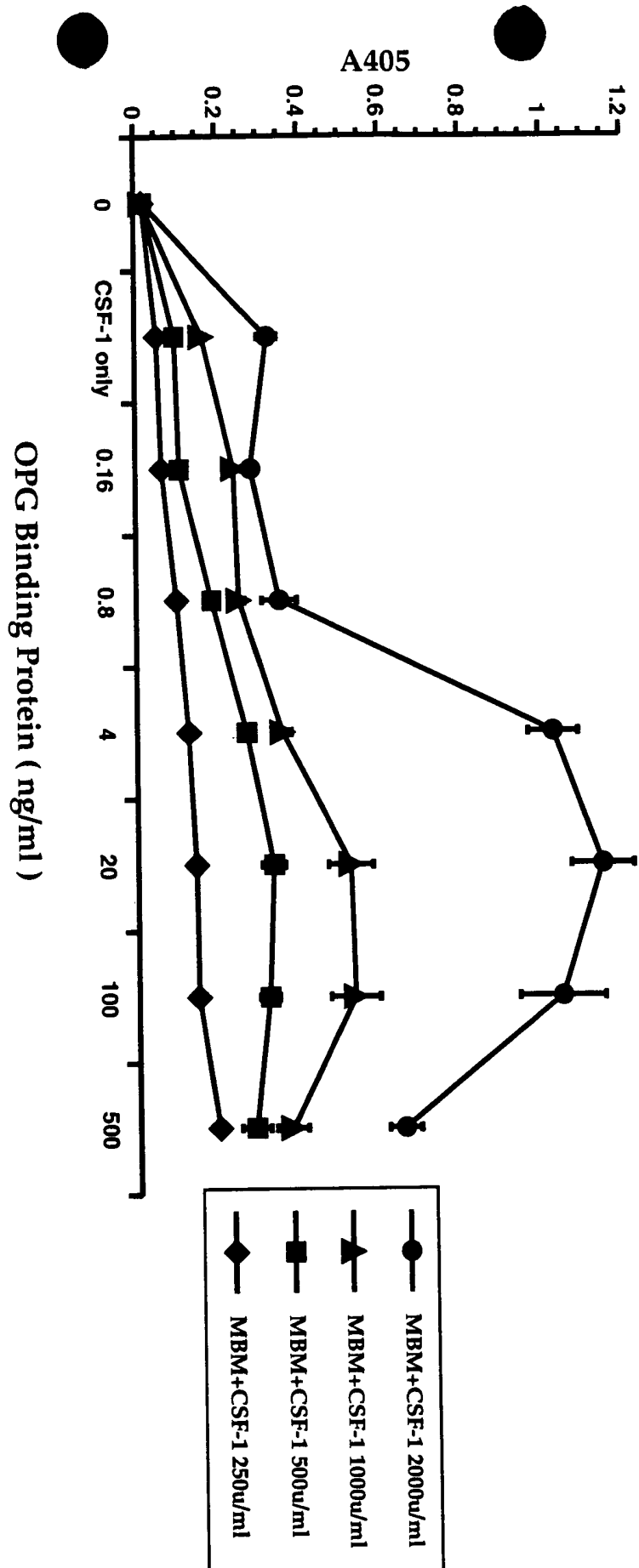
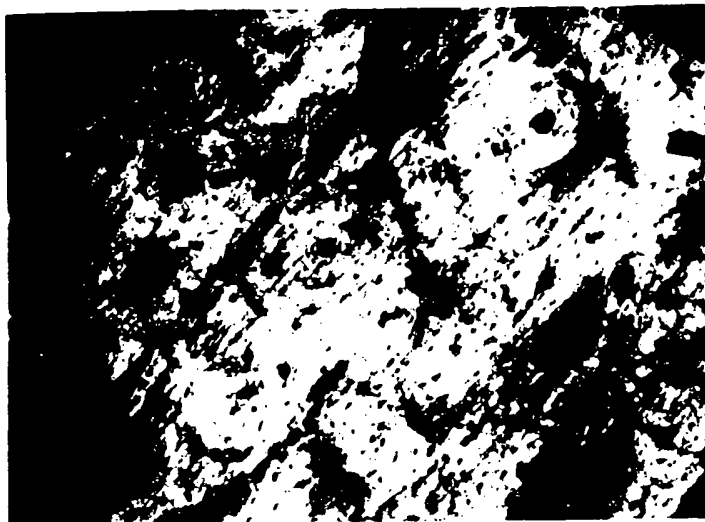


FIGURE 6

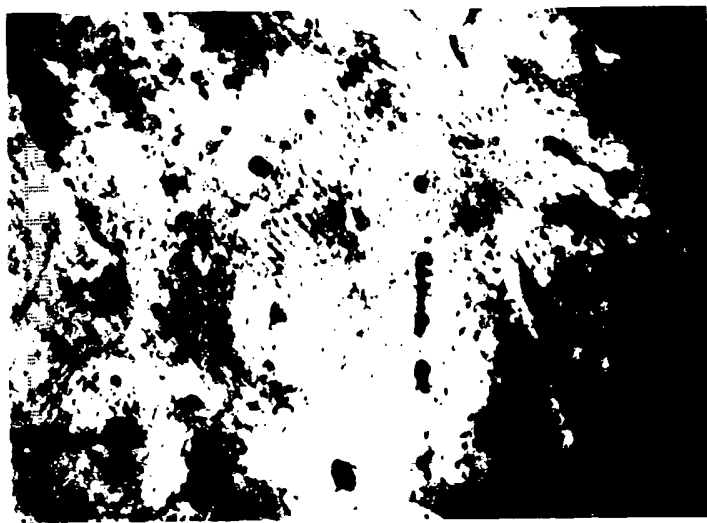
**Toluidine Blue Staining**



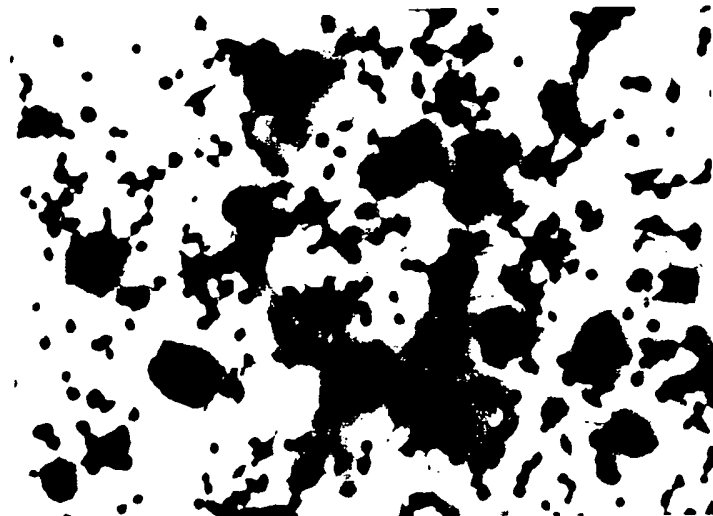
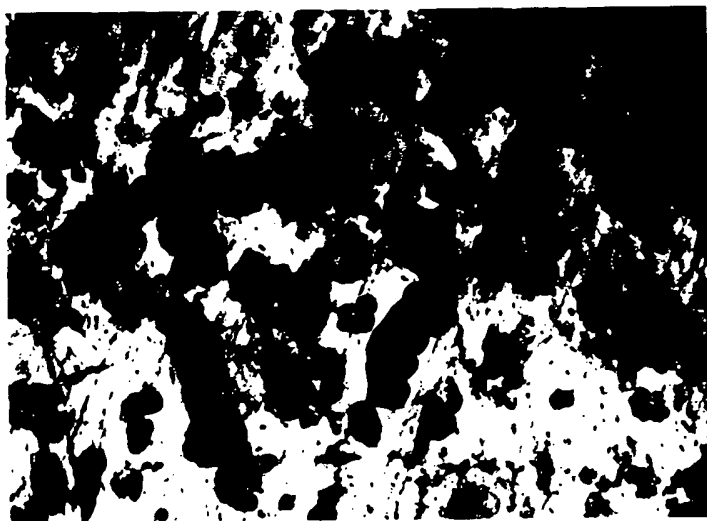
**AP staining**



**Bone Marrow Cells + M-CSF-1**



**Bone Marrow Cells + OPG Binding Protein**



**Bone Marrow Cells + M-CSF-1 + OPG Binding Protein**

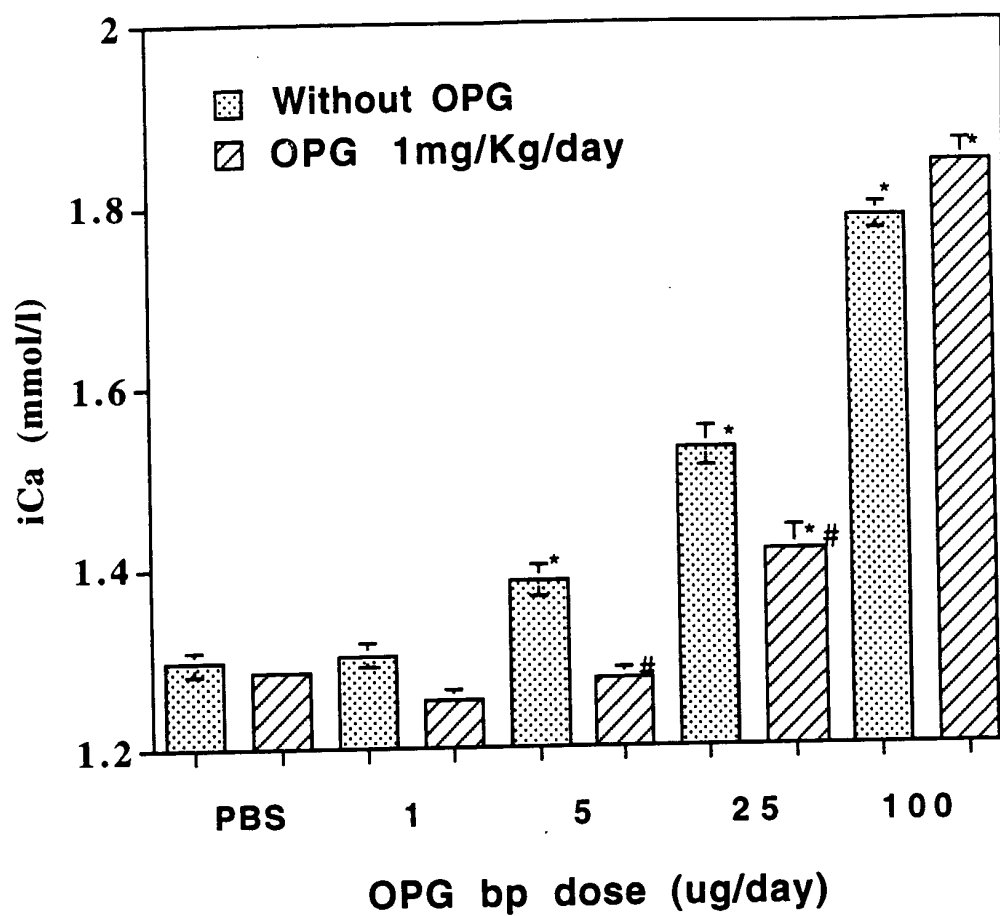


FIGURE 8

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B64T 260

**PBS**



**OPGbp 5ug/d**



**OPGbp 25ug/d**



**OPGbp100ug/d**



FIGURE 9